**S2 Table: Mean absolute error (MAE) segmentation regression estimates following cross-validation along with use of lesion masks (mean** $\pm $ **sd).**

|  |  |  |
| --- | --- | --- |
| **Tissue** | **Blue (Myelin)** | **Red (Cellularity)** |
| **Intercept** | **Slope** | **Intercept** | **Slope** |
| SG | $$0.22\pm 0.22$$ | $$0.04\pm 0.25$$ | $$0.75\pm 0.13$$ | $$0.03\pm 0.14$$ |
| GM | $$0.782\pm 0.037$$ | $$-0.566\pm 0.051$$ | $$0.32\pm 0.15$$ | $$0.46\pm 0.20$$ |
| PV | $$2.05\pm 0.19$$ | $$-2.28\pm 0.28$$ | $$-1.15\pm 0.43$$ | $$2.43\pm 0.64$$ |
| WM | $$0.854\pm 0.087$$ | $$-0.20\pm 0.16$$ | $$0.13\pm 0.11$$ | $0.16\pm 0.2$0 |
| Lesion | $$0.183\pm 0.053$$ | $$0.158\pm 0.058$$ | $$1.210\pm 0.040$$ | $$-0.422\pm 0.055$$ |